

10/565438

LISTE DE SEQUENCES

<110> Centre National de la Recherche Scientifique IAP20 Rec'd FEB/03 20 JAN 2006

<120> Peptide inhibiteur de la traduction des protéines et
utilisation pour le contrôle de la traduction des
protéines

<130> P290-FR

<140>
<141>

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 28
<212> PRT
<213> Xenopus laevis<400> 1
Val Lys Phe Ala Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr
1 5 10 15

Gln Gln Leu Gln Gln Gln Met Gln Gln Leu Asn Ala
20 25<210> 2
<211> 28
<212> PRT
<213> Homo sapiens<400> 2
Val Lys Phe Ala Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala
1 5 10 15

Gln Gln Leu Gln Gln Gln Met Gln Gln Ile Ser Ala
20 25<210> 3
<211> 84
<212> PRT
<213> Xenopus laevis<400> 3
Phe Thr Thr Arg Ser Met Ala Gln Met Ala Ile Lys Ser Met His Gln
1 5 10 15

Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala
20 25 30

Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
35 40 45

Gln Gln Met Gln Gln Leu Asn Ala Ala Ser Met Trp Gly Asn Leu Thr

50 55 60

Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr
 65 70 75 80
 Ala Ser Ser Gly

<210> 4
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 4
 Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met His Gln
 1 5 10 15

Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala
 20 25 30

Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln
 35 40 45

Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala
 50 55 60

Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu
 65 70 75 80

Leu Gln Gln Thr Ala Ser Ser Gly
 85

<210> 5
 <211> 189
 <212> PRT
 <213> Séquence artificielle

<220>
 <223> Description de la séquence artificielle:fusion

<400> 5
 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala
 1 5 10 15

Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
 20 25 30

Gln Gln Met Gln Gln Leu Asn Ala Ala Ala Ala Met Ala Ser Asn Phe
 35 40 45

Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr Gly Asp Val Thr Val
 50 55 60

Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp Ile Ser Ser Asn
 65 70 75 80

Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val Arg Gln Ser Ser

85

90

95

Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val Pro Lys Val Ala
 100 105 110

Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val Ala Gly Trp Arg Ser
 115 120 125

Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala Thr Asn Ser Asp
 130 135 140

Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu Lys Asp Gly Asn
 145 150 155 160

Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile Tyr Gly Gly Gly
 165 170 175

Gly Gly Ser Gly Pro Tyr Ser Ile Val Ser Pro Lys Cys
 180 185

<210> 6

<211> 154

<212> PRT

<213> Séquence artificielle

<220>

<223> Description de la séquence artificielle:fusion

<400> 6

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val
 65 70 75 80

Ala Gly Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro
 130 135 140

Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala
 145 150

```

<210> 7
<211> 570
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:fusion

<400> 7
atggcttacc catacgatgt tccagattac gctagcgtaa agttcgcaga cactcagaaa 60
gacaaagaac agaagcgcat gacgcagcaa cttcagcagc aaatgcagca gctcaatgca 120
gcggccgcca tggcttctaa ctttactcgat ttcgttctcg tcgacaatgg cggaactggc 180
gacgtgactg tcgccccaaag caacttcgct aacggggtcg ctgaatggat cagctctaac 240
tcgcgatcac aggcttacaa agtaaacctgt agcggttcgtc agagctctgc gcagaatcgc 300
aaatacacca tcaaaggatcga ggtgcctaaa gtggcaaccc agactgttgg tggtaagag 360
cttcctgttag ccggatggag atcttactta aatatggAAC taaccattcc aattttcgcc 420
acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
ccctattcta tagtgtcacc taaatgctag 570

<210> 8
<211> 570
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:fusion

<400> 8
atggcttacc catacgatgt tccagattac gctagcgtaa aatttgctga tacacagaag 60
gacaaagaac agaagagaat ggcccagcag ctccagcagc agatgcagca aatcagcgc 120
gcggccgcca tggcttctaa ctttactcgat ttcgttctcg tcgacaatgg cggaactggc 180
gacgtgactg tcgccccaaag caacttcgct aacggggtcg ctgaatggat cagctctaac 240
tcgcgatcac aggcttacaa agtaaacctgt agcggttcgtc agagctctgc gcagaatcgc 300
aaatacacca tcaaaggatcga ggtgcctaaa gtggcaaccc agactgttgg tggtaagag 360
cttcctgttag ccggatggag atcttactta aatatggAAC taaccattcc aattttcgcc 420
acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
ccctattcta tagtgtcacc taaatgctag 570

<210> 9
<211> 489
<212> PRT
<213> Xenopus laevis

<400> 9
Met Asn Gly Thr Met Asp His Pro Asp His Pro Asp Pro Asp Ser Ile
    1          5           10          15

Lys Met Phe Val Gly Gln Val Pro Arg Ser Trp Ser Glu Lys Glu Leu
    20         25           30

Arg Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu
    35         40           45

Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Ile
    50         55           60

```

Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala Leu His
 65 70 75 80
 Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln Met Lys Pro
 85 90 95
 Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg Lys Leu Phe Ile
 100 105 110
 Gly Met Val Ser Lys Asn Cys Asn Glu Asn Asp Ile Arg Ala Met Phe
 115 120 125
 Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg Gly Pro Asp
 130 135 140
 Gly Met Ser Arg Gly Cys Ala Phe Val Thr Phe Thr Thr Arg Ser Met
 145 150 155 160
 Ala Gln Met Ala Ile Lys Ser Met His Gln Ala Gln Thr Met Glu Gly
 165 170 175
 Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln Lys Asp Lys
 180 185 190
 Glu Gln Lys Arg Met Thr Gln Gln Leu Gln Gln Met Gln Gln Leu
 195 200 205
 Asn Ala Ala Ser Met Trp Gly Asn Leu Thr Gly Leu Asn Ser Leu Ala
 210 215 220
 Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn Leu
 225 230 235 240
 Asn Ser Leu Ser Gly Leu His Pro Met Gly Ala Glu Tyr Gly Thr Gly
 245 250 255
 Met Thr Ser Gly Leu Asn Ala Ile Gln Leu Gln Asn Leu Ala Ala Leu
 260 265 270
 Ala Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala
 275 280 285
 Leu Thr Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser
 290 295 300
 Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly
 305 310 315 320
 Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser
 325 330 335
 Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser
 340 345 350
 Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly
 355 360 365
 Ile Gln Gln Tyr Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser
 370 375 380

Leu	Leu	Ser	Gln	Gln	Gly	Leu	Gly	Ala	Ala	Gly	Ser	Gln	Lys	Glu	Gly
385					390					395					400
Pro	Glu	Gly	Ala	Asn	Leu	Phe	Ile	Tyr	His	Leu	Pro	Gln	Glu	Phe	Gly
	405							410							415
Asp	Gln	Asp	Leu	Leu	Gln	Met	Phe	Met	Pro	Phe	Gly	Asn	Val	Val	Ser
		420						425							430
Ser	Lys	Val	Phe	Ile	Asp	Lys	Gln	Thr	Asn	Leu	Ser	Lys	Cys	Phe	Gly
		435					440								445
Phe	Val	Ser	Tyr	Asp	Asn	Pro	Val	Ser	Ala	Gln	Ala	Ala	Ile	Gln	Ser
		450					455								460
Met	Asn	Gly	Phe	Gln	Ile	Gly	Met	Lys	Arg	Leu	Lys	Val	Gln	Leu	Lys
		465					470								480
Arg	Ser	Lys	Asn	Asp	Ser	Lys	Pro	Tyr							
				485											

<210> 10
<211> 1470
<212> ADN
<213> Xenopus laevis

<400> 10

```

atgaatggca caatggacca cccagaccat ccggatccgg actccatcaa gatgtttgtg 60
ggtcagggtc ctcgaagctg gtcatggaaaa gagctaagag aactcttcga gcagtacgga 120
gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180
tgctgttta ttactttcta cacaagaaaa gctgcgttag aagcacagaa tgctttgcac 240
aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtgaa 300
aagaataatg ctgtggaaaga ccgaaagcta tttatcgaa tggtttccaa gaattgtaat 360
gagaatgata tccggccat gttctctccg tttggacaga tagaggaatg tcgtatcctg 420
cgaggcccctg atgaaatgag cagaggatgt gcattcgta cgtttacaac tagatccatg 480
gcacagatgg caatcaaatac catgcaccaa gcacaaaacca tggagggctg ttcctcacca 540
atagtggtaa agttcgcaga cactcgaaaa gacaaagaac agaaagcgcac gacgcagcaa 600
cttcagcagc aaatgcagca gctcaatgca gcctcaatgt gggtaacct gactggactg 660
aacagcttgg caccggcata tttagcactc ctccagcaga ccgcctccctc tgggaacctc 720
aactccctaa gtggtctcca ccctatggga gctgagtagc gcactggaaat gacatcagg 780
cttaatgcca tacagttaca gaatttggca gctttagcgg ctgctgctag tgctgcgcag 840
aacaccccaa gtgcaggagc agcgctact tcttccagca gccccctcag catcctaacc 900
agtcccggtt cctcccccaag ttcaaataac tcatccatca acaccatggc atccctagga 960
gctctacaga cattggctgg ggcacacagct ggtctcaatg tcaattcgct tgcaggtatg 1020
gctgcgttta atggaggcct aggcagcagt ctctccatg gcactggcag tacgatggaa 1080
gcccttagtc aagtttactc tgggattcag cagttatgtc ccgctgcact tccttcaactc 1140
tataaccaga gcctttgtc acaacagggt ttggggctg cggggagtc gaaagaaggc 1200
ccagaaggag ccaacccccc tatataccac ctacccagg agttggggaa ccaggatctc 1260
ctgcagatgt tcatgccatt tggaaatgtt gtgtccctca aagttttcat cgacaaacaa 1320
acgaacccctca gcaaatgttt tggcttcgtt agttacgaca atcccgatc tgctcaggct 1380
gctatccagt ccatgaacgg ctttcagatc ggaatgaaac gcctgaaagt ccaactcaaa 1440
cgctccaaaga atgacagcaa accctactga
```

1470

<210> 11
<211> 9
<212> PRT
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:peptide HA

<400> 11
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 12
<211> 33
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:amorce

<400> 12
atgctagcgt aaagttcgca gacactcaga aag

33

<210> 13
<211> 32
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:amorce

<400> 13
atgcggccgc tgcattgagc tgctgcattt gc

32

<210> 14
<211> 32
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:amorce

<400> 14
atgctagcgt aaaatttgct gatacacaga ag

32

<210> 15
<211> 32
<212> ADN
<213> Séquence artificielle

<220>
<223> Description de la séquence artificielle:amorce

<400> 15
atgcggccgc tgcgctgatt tgctgcattc gc

32

<210> 16
<211> 27
<212> ADN
<213> Séquence artificielle

<220>

<223> Description de la séquence artificielle:peptide HA

<400> 16

tacccatacg atgttccaga ttacgct

27